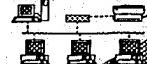


*04 CO 12-08-00*

## RAW SEQUENCE LISTING ERROR REPORT

BIOTECHNOLOGY  
SYSTEMS  
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/738,444

Source: OIPE

Date Processed by STIC: 01-08-01

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin30help@uspto.gov](mailto:patin30help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

### **Checker Version 3.0**

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

# Raw Sequence Listing Error Summary

## ERROR DETECTED    SUGGESTED CORRECTION

SERIAL NUMBER: 09/738,444

| ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE |  |
|--|--|
| 1 <input type="checkbox"/> Wrapped Nucleic   | The number/text at the end of each line "wrapped" down to the next line.<br>This may occur if your file was retrieved in a word processor after creating it.<br>Please adjust your right margin to .3, as this will prevent "wrapping".  |
| 2 <input type="checkbox"/> Wrapped Aminos  | The amino acid number/text at the end of each line "wrapped" down to the next line.<br>This may occur if your file was retrieved in a word processor after creating it.<br>Please adjust your right margin to .3, as this will prevent "wrapping".   |
| 3 <input type="checkbox"/> Incorrect Line Length   | The rules require that a line not exceed 72 characters in length. This includes spaces.  |
| 4 <input type="checkbox"/> Misaligned Amino Acid Numbering   | The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.  |
| 5 <input type="checkbox"/> Non-ASCII   | This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.<br>Please ensure your subsequent submission is saved in ASCII text so that it can be processed.  |
| 6 <input type="checkbox"/> Variable Length   | Sequence(s) _____ contain n's or Xaa's which represented more than one residue.<br>As per the rules, each n or Xaa can only represent a single residue.<br>Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.   |
| 7 <input type="checkbox"/> PatentIn ver. 2.0 "bug"   | A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.           |
| 8 <input type="checkbox"/> Skipped Sequences (OLD RULES)   | Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:<br>(2) INFORMATION FOR SEQ ID NO:X:<br>(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")<br>(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:<br><b>This sequence is intentionally skipped</b><br><br>Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s). |
| 9 <input type="checkbox"/> Skipped Sequences (NEW RULES)   | Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.<br><210> sequence id number<br><400> sequence id number<br>000   |
| 10 <input type="checkbox"/> Use of n's or Xaa's (NEW RULES)  | Use of n's and/or Xaa's have been detected in the Sequence Listing.<br>Use of <220> to <223> is MANDATORY if n's or Xaa's are present.<br>In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.   |
| 11 <input type="checkbox"/> Use of <213>Organism (NEW RULES)   | Sequence(s) _____ are missing this mandatory field or its response.<br><br>/-14  |
| 12 <input checked="" type="checkbox"/> Use of <220>Feature (NEW RULES)                               | Sequence(s) _____ are missing the <220>Feature and associated headings.<br>Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"<br><u>Please explain source of genetic material in &lt;220&gt; to &lt;223&gt; section.</u><br>(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)    (Sec. 1.823 of new Rules)   |
| 13 <input type="checkbox"/> PatentIn ver. 2.0 "bug"  | Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.   |

OIPE

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/738,444  
 Input Set : A:\Neb-180.app  
 Output Set: N:\CRF3\01082001\I738444.raw

DATE: 01/08/2001  
 TIME: 14:19:40

Does Not Comply  
 Corrected Diskette Needed  
 See pp. 1-2

```

3 <110> APPLICANT: Jack, William E.
4      Schildkraut, Ira
5      Menin, Julie F.
6      Greenough, Lucia
8 <120> TITLE OF INVENTION: Use of Site-Specific Nicking Endonucleases to Create
9      Single-Stranded Regions And Applications Thereof
11 <130> FILE REFERENCE: NEB-180
C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/738,444
C--> 14 <141> CURRENT FILING DATE: 2000-12-15
16 <160> NUMBER OF SEQ ID NOS: 51
18 <170> SOFTWARE: PatentIn Ver. 2.0
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 40
22 <212> TYPE: DNA
23 <213> ORGANISM: synthetic oligonucleotide
25 <400> SEQUENCE: 1
26 aaatcaatct aaagtatata ccggtaaact tggctgaca
28 <210> SEQ ID NO: 2
29 <211> LENGTH: 38
30 <212> TYPE: DNA
31 <213> ORGANISM: synthetic oligonucleotide
33 <400> SEQUENCE: 2
34 ctagcattag tcagactcta cattcaaata tgtatccg
36 <210> SEQ ID NO: 3
37 <211> LENGTH: 38
38 <212> TYPE: DNA
39 <213> ORGANISM: synthetic oligonucleotide
41 <400> SEQUENCE: 3
42 ggcgtcgatg tcagactcga gcaaaaggcc agcaaaaag
44 <210> SEQ ID NO: 4
45 <211> LENGTH: 56
46 <212> TYPE: DNA
47 <213> ORGANISM: synthetic oligonucleotide
49 <400> SEQUENCE: 4
50 gagtcggatt gacctaagcg gatactctga cgactcgtag aaaaatcaa aggatac
52 <210> SEQ ID NO: 5
53 <211> LENGTH: 51
54 <212> TYPE: DNA
55 <213> ORGANISM: synthetic oligonucleotide
57 <400> SEQUENCE: 5
58 gagtctcaaga ctatctggag cgactqactc aaacttggtc tgacagttac c
60 <210> SEQ ID NO: 6
61 <211> LENGTH: 40
62 <212> TYPE: DNA
63 <213> ORGANISM: synthetic oligonucleotide
65 <400> SEQUENCE: 6
66 gtaaaatatcg gactctacaa tcaaatatgt atccgctat

```

Valid responses for <213>:

- Genus species
- Artificial Sequence
- Unknown sequence

Also missing  
 mandatory <220>, <23>  
 features to explain  
 source of artificial  
 sequences

See #12 on the  
 Error Summary Sheet.

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/738,444

DATE: 01/08/2001  
TIME: 14:19:40

Input Set : A:\Neb-180.app  
Output Set: N:\CRF3\01082001\I738444.raw

```

68 <210> SEQ ID NO: 7
69 <211> LENGTH: 82
70 <212> TYPE: DNA
71 <213> ORGANISM: synthetic oligonucleotide
73 <400> SEQUENCE:
74 gatcgagtc gacatcgacgc gccttagcatt agtcagactc gatacgggt ctcaaggctgt 60
75 taacgatgtt acatgcacgc tc 82
77 <210> SEQ ID NO: 8
78 <211> LENGTH: 82
79 <212> TYPE: DNA
80 <213> ORGANISM: synthetic oligonucleotide
82 <400> SEQUENCE:
83 cttagggatcg tcatgttacca tcgttaaacatg gctggagactc gatacgggt ctgactaaatg 60
84 cttaggcgttc gatgtcagac tc 82
86 <210> SEQ ID NO: 9
87 <211> LENGTH: 22
88 <212> TYPE: DNA
89 <213> ORGANISM: synthetic oligonucleotide
91 <400> SEQUENCE:
92 catgtctaga ctgcagagat ct 22
94 <210> SEQ ID NO: 10
95 <211> LENGTH: 18
96 <212> TYPE: DNA
97 <213> ORGANISM: synthetic oligonucleotide
99 <400> SEQUENCE:
100 agatctctgc agtctaga 18
102 <210> SEQ ID NO: 11
103 <211> LENGTH: 21
104 <212> TYPE: DNA
105 <213> ORGANISM: synthetic oligonucleotide
107 <400> SEQUENCE:
108 tacattcaa tatgtatccg c 21
110 <210> SEQ ID NO: 12
111 <211> LENGTH: 21
112 <212> TYPE: DNA
113 <213> ORGANISM: synthetic oligonucleotide
115 <400> SEQUENCE:
116 taaacttggt ctgacagttt c 21
118 <210> SEQ ID NO: 13
119 <211> LENGTH: 54
120 <212> TYPE: DNA
121 <213> ORGANISM: synthetic oligonucleotide
123 <400> SEQUENCE:
124 gagttatccgc ttatggtaat ccggactccga ccggatataca catgtggatgc gtca 54
126 <210> SEQ ID NO: 14
127 <211> LENGTH: 54
128 <212> TYPE: DNA
129 <213> ORGANISM: synthetic oligonucleotide
131 <400> SEQUENCE:

```

refer to P<sup>1</sup>

Error #12

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/738,444

DATE: 01/08/2001  
TIME: 14:19:40

Input Set : A:\Neb-180.app  
Output Set: N:\CRF3\01082001\I738444.raw

```

132 cctgttageg atggacatcg acgactcaca tgtgatatcc ggtccgagtc cgat      54
134 <210> SEQ ID NO: 15
135 <211> LENGTH: 10
136 <212> TYPE: DNA
137 <213> ORGANISM: N.BSTNBT Recognition Sequence
139 <220> FEATURE:
140 <223> OTHER INFORMATION: N indicates any base (subject to the normal rules
141      of base pairing between the strands).
143 <400> SEQUENCE: 15
W--> 144 gagtcnnnnn                                         10
145 <210> SEQ ID NO: 16
147 <211> LENGTH: 18
148 <212> TYPE: DNA
149 <213> ORGANISM: Artificial Sequence
151 <220> FEATURE:
152 <223> OTHER INFORMATION: Description of Artificial Sequence: Theoretical
153      sequences - all randomly generated
155 <400> SEQUENCE: 16
156 ggcgtttaaac ccagatgt
158 <210> SEQ ID NO: 17
159 <211> LENGTH: 18
160 <212> TYPE: DNA
161 <213> ORGANISM: Artificial Sequence
163 <220> FEATURE:
164 <223> OTHER INFORMATION: Description of Artificial Sequence: Theoretical
165      sequences - all randomly generated
167 <400> SEQUENCE: 17
168 gcgttcaaac ccagatgt                                         18
170 <210> SEQ ID NO: 18
171 <211> LENGTH: 18
172 <212> TYPE: DNA
173 <213> ORGANISM: Artificial Sequence
175 <220> FEATURE:
176 <223> OTHER INFORMATION: Description of Artificial Sequence: Theoretical
177      sequences - all randomly generated
179 <400> SEQUENCE: 18
180 agctgtttcta agccqcaa                                         18
182 <210> SEQ ID NO: 19
183 <211> LENGTH: 18
184 <212> TYPE: DNA
185 <213> ORGANISM: Artificial Sequence
187 <220> FEATURE:
188 <223> OTHER INFORMATION: Description of Artificial Sequence: Theoretical
189      sequences - all randomly generated
191 <400> SEQUENCE: 19
192 tgtgaacacc tctgttaacg                                         18
194 <210> SEQ ID NO: 20
195 <211> LENGTH: 18
196 <212> TYPE: DNA

```

OK

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/738,444

DATE: 01/03/2001  
TIME: 14:19:40

Input Set : A:\Neb-180.app  
Output Set: N:\CRF3\01082001\1738444.raw

197 <213> ORGANISM: Artificial Sequence  
199 <220> FEATURE:  
200 <223> OTHER INFORMATION: Description of Artificial Sequence: Theoretical  
201 sequences - all randomly generated.  
203 <400> SEQUENCE: 20  
204 ttcccaagca catggat 18  
206 <210> SEQ ID NO: 21  
207 <211> LENGTH: 18  
208 <212> TYPE: DNA  
209 <213> ORGANISM: Artificial Sequence  
211 <220> FEATURE:  
212 <223> OTHER INFORMATION: Description of Artificial Sequence: Theoretical  
213 sequences - all randomly generated  
215 <400> SEQUENCE: 21  
216 ttcccaagca cagtgat 18  
218 <210> SEQ ID NO: 22  
219 <211> LENGTH: 18  
220 <212> TYPE: DNA  
221 <213> ORGANISM: Artificial Sequence  
223 <220> FEATURE:  
224 <223> OTHER INFORMATION: Description of Artificial Sequence: Theoretical  
225 sequences - all randomly generated  
227 <400> SEQUENCE: 22  
228 tgactcaagg gatgtac 18  
230 <210> SEQ ID NO: 23  
231 <211> LENGTH: 18  
232 <212> TYPE: DNA  
233 <213> ORGANISM: Artificial Sequence  
235 <220> FEATURE:  
236 <223> OTHER INFORMATION: Description of Artificial Sequence: Theoretical  
237 sequences - all randomly generated  
239 <400> SEQUENCE: 23  
240 tgactcaagg ggatactc 18  
242 <210> SEQ ID NO: 24  
243 <211> LENGTH: 18  
244 <212> TYPE: DNA  
245 <213> ORGANISM: Artificial Sequence  
247 <220> FEATURE:  
248 <223> OTHER INFORMATION: Description of Artificial Sequence: Theoretical  
249 sequences - all randomly generated  
251 <400> SEQUENCE: 24  
252 tgcataagg ggataactc 18  
254 <210> SEQ ID NO: 25  
255 <211> LENGTH: 18  
256 <212> TYPE: DNA  
257 <213> ORGANISM: Artificial Sequence  
259 <220> FEATURE:  
260 <223> OTHER INFORMATION: Description of Artificial Sequence: Theoretical  
261 sequence - randomly generated

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/738,444

DATE: 01/08/2001  
TIME: 14:19:40

Input Set : A:\Neb-180.app  
Output Set: N:\CRF3\01082001\I738444.raw

263 <400> SEQUENCE: 25  
264 atcgagcgcc atgcattta 18  
266 <210> SEQ ID NO: 26  
267 <211> LENGTH: 18  
268 <212> TYPE: DNA  
269 <213> ORGANISM: Artificial Sequence  
271 <220> FEATURE:  
272 <223> OTHER INFORMATION: Description of Artificial Sequence: Theoretical  
sequence - randomly generated  
273 sequence: 26  
275 <400> SEQUENCE: 26  
276 atcgaggccc agtcattta 18  
278 <210> SEQ ID NO: 27  
279 <211> LENGTH: 18  
280 <212> TYPE: DNA  
281 <213> ORGANISM: Artificial Sequence  
283 <220> FEATURE:  
284 <223> OTHER INFORMATION: Description of Artificial Sequence: Theoretical  
sequence - randomly generated  
285 sequence: 27  
287 <400> SEQUENCE: 27  
288 atcgaggccc atgcattta 18  
290 <210> SEQ ID NO: 28  
291 <211> LENGTH: 18  
292 <212> TYPE: DNA  
293 <213> ORGANISM: Artificial Sequence  
295 <220> FEATURE:  
296 <223> OTHER INFORMATION: Description of Artificial Sequence: Theoretical  
sequence - randomly generated  
297 sequence: 28  
299 <400> SEQUENCE: 28  
300 atcgagcgcc tagcattta 18  
302 <210> SEQ ID NO: 29  
303 <211> LENGTH: 18  
304 <212> TYPE: DNA  
305 <213> ORGANISM: Artificial Sequence  
307 <220> FEATURE:  
308 <223> OTHER INFORMATION: Description of Artificial Sequence: Theoretical  
sequence - randomly generated  
309 sequence: 29  
311 <400> SEQUENCE: 29  
312 ttttaccatcg ctaacagg 18  
314 <210> SEQ ID NO: 30  
315 <211> LENGTH: 36  
316 <212> TYPE: DNA  
317 <213> ORGANISM: Artificial Sequence  
319 <220> FEATURE:  
320 <223> OTHER INFORMATION: Description of Artificial Sequence: Theoretical  
sequence - implemented via the synthetic  
322 oligonucleotide, but never existed as independent  
323 entity  
325 <400> SEQUENCE: 30  
326 gatgtctgaca tcgagcgctt agcatttagtc agactc 36

VERIFICATION SUMMARY  
PATENT APPLICATION: US/09/738,444 DATE: 01/08/2001  
TIME: 14:19:41

Input Set : A:\Neb-180.app  
Output Set: N:\CRF3\01082001\1738444.raw

L:13 M:270 C: Current Application Number differs, Replaced Application Number  
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:144 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:15  
L:144 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:15  
L:144 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:15